



In silico prediction of the emergent effects of drugs on cardiac electrical activity

Colleen E. Clancy Lab

*“In few specialties of medicine
are new promising drugs shown
to be so much inferior to
placebo, and even worse, to
increase mortality.”*

-Sanderson, 1996 [Editorial on SWORD and CAST trials]

...But this doesn't mean that these drugs can't be useful in **some** situations

There is currently no reliable method to predict when antiarrhythmic drugs will succeed or fail.

NEW technologies for pharmacology

PatchExpress and Ionworks NMR Screening

Synthetic biology

Novel Reagents

Biosensors

Patient-derived pluripotent stem (iPS) cells

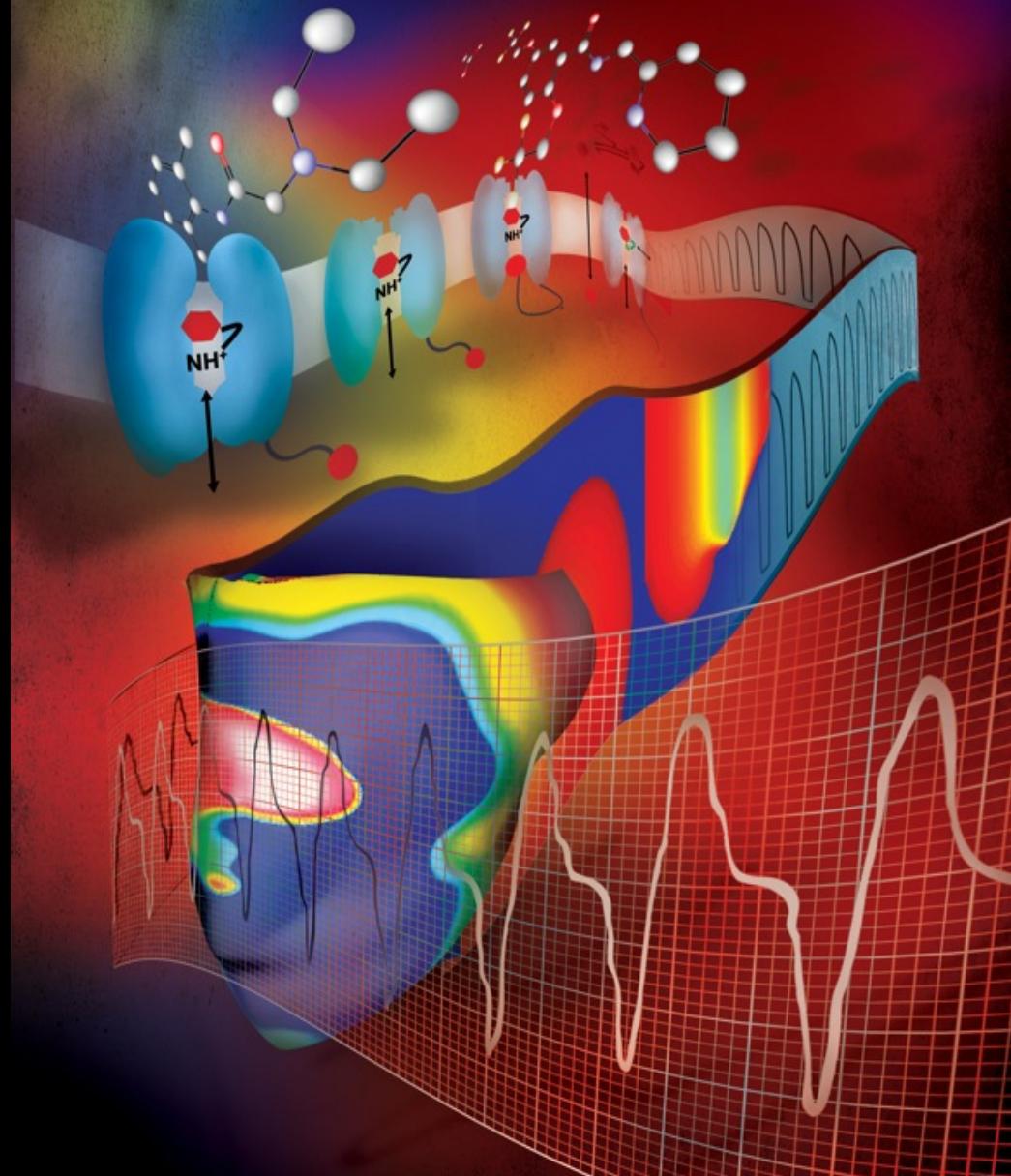
It's EXCITING!

BUT.....

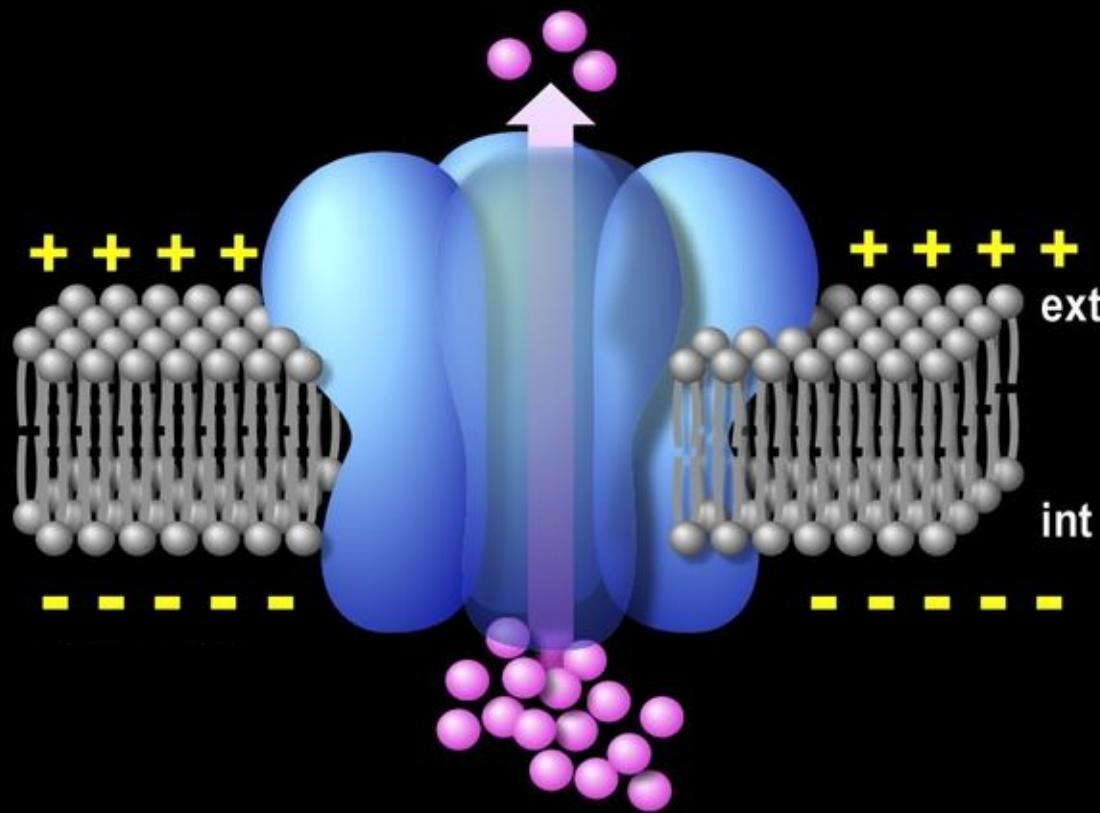
While all of these developing technologies are innovative and needed, they ***focus only on constituent elements*** of the system. They can't each alone solve the fundamental problem – that the effects of multifaceted drug interactions are ***emergent.***

Our goal

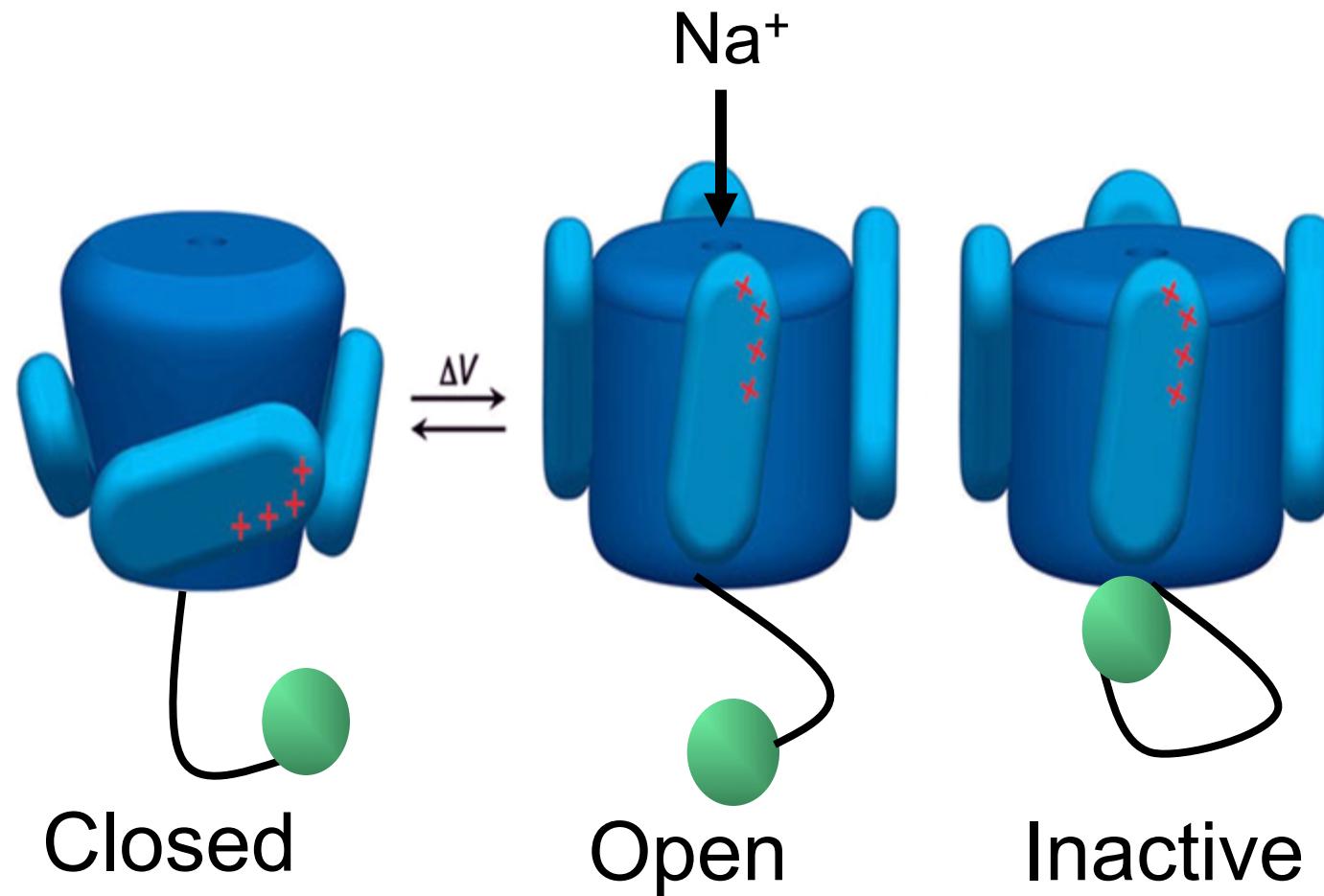
Develop a computational processes for **SCREENING** for drug and disease, determination of **MECHANISMS** of success and failure and prediction of **THERAPY**



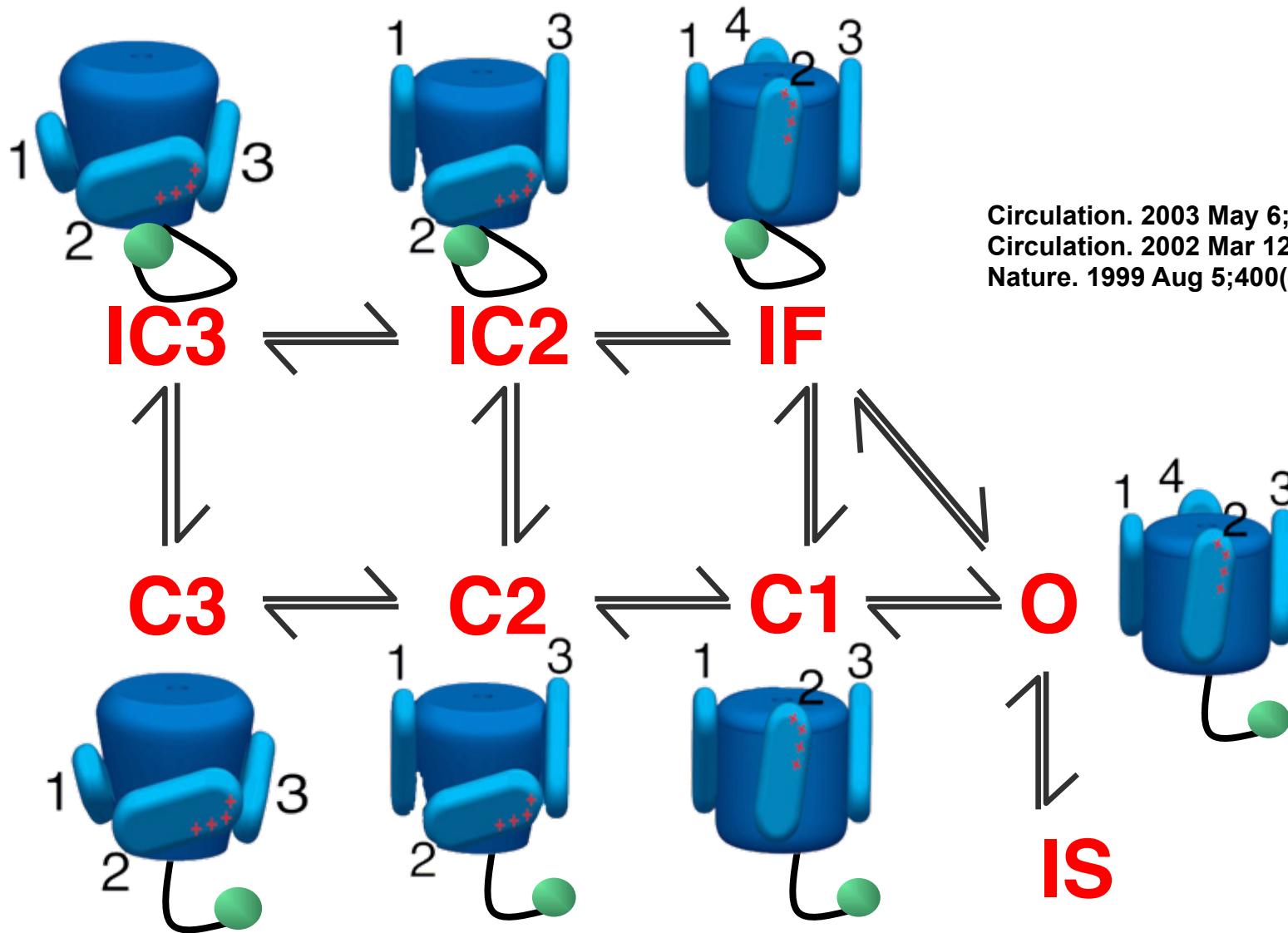
Most drugs intended to treat cardiac arrhythmia block voltage gated ion channels



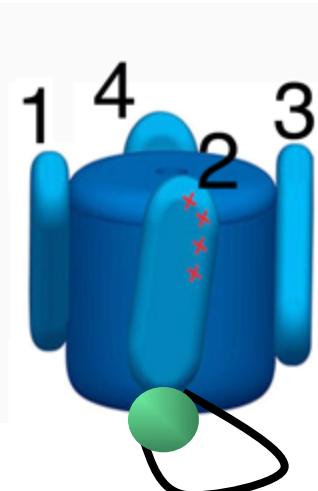
Modeling drug free cardiac I_{Na} (encoded by SCN5A)



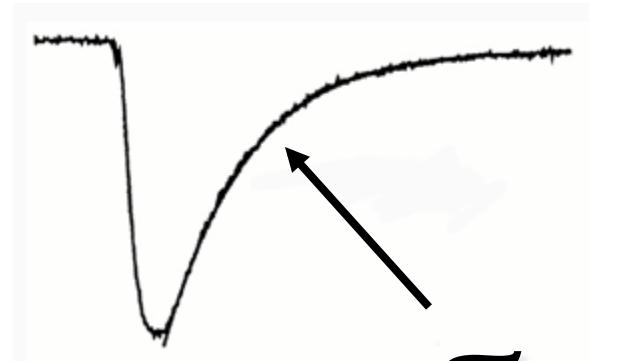
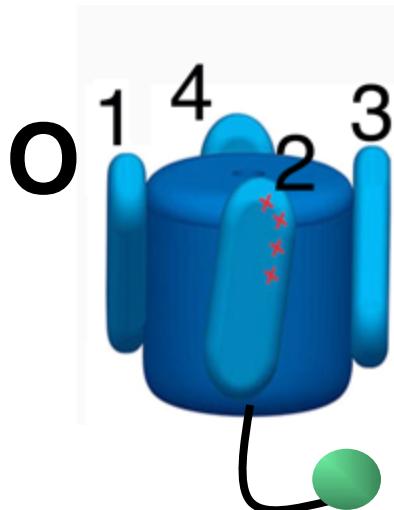
A computational model that predicts Na^+ channel kinetics



Extracting model parameters from experimental data

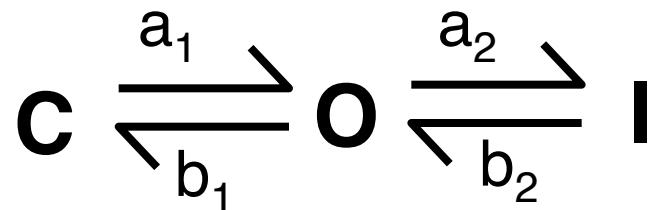


IF
 α



$$\tau_{decay} = 1 / \alpha$$

Computation of state probabilities



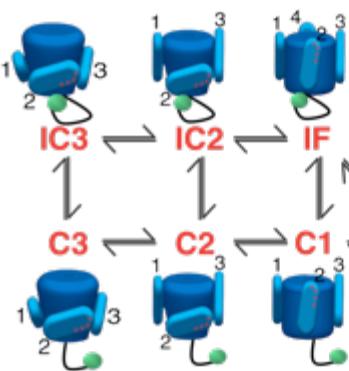
$$\frac{dP_i}{dt} = \sum_{j=1}^N [k_{ji} \bullet P_j(t, V_m)] - \sum_{j=1}^N [k_{ij} \bullet P_i(t, V_m)]$$

$$dC/dt = P(O) \cdot b_1 - P(C) \cdot a_1$$

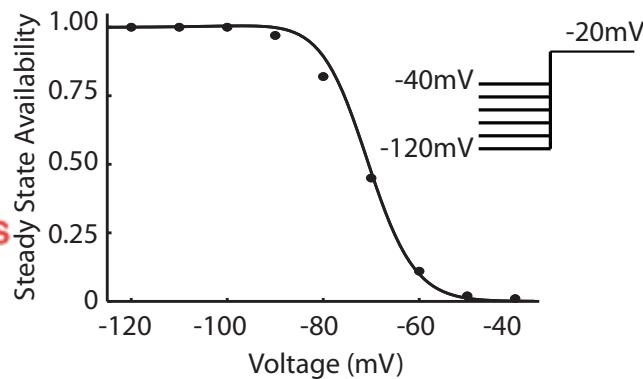
$$dO/dt = P(C) \cdot b_1 + P(I) \cdot b_2 - (P(O) \cdot (a_2 + b_1))$$

$$dI/dt = P(O) \cdot a_2 - P(I) \cdot b_2$$

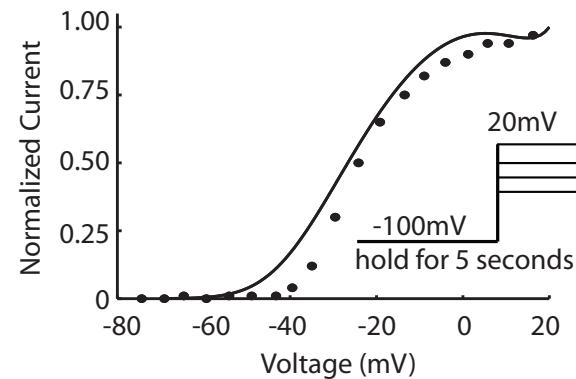
Wild-type Drug Free Model - *Postoptimization*



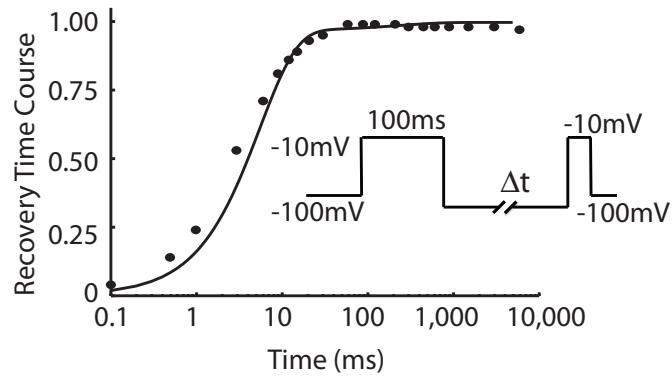
a.



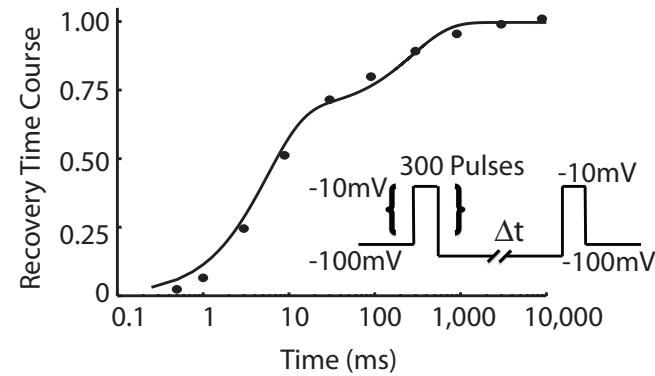
b.



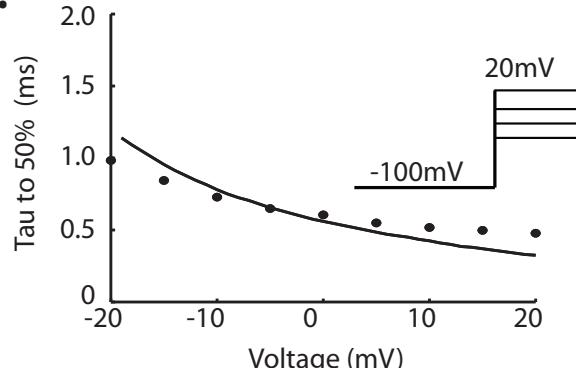
c.



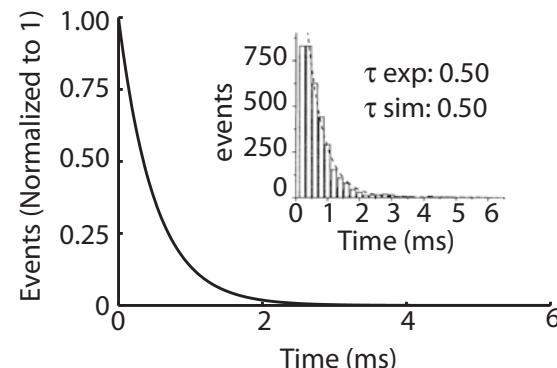
d.



e.

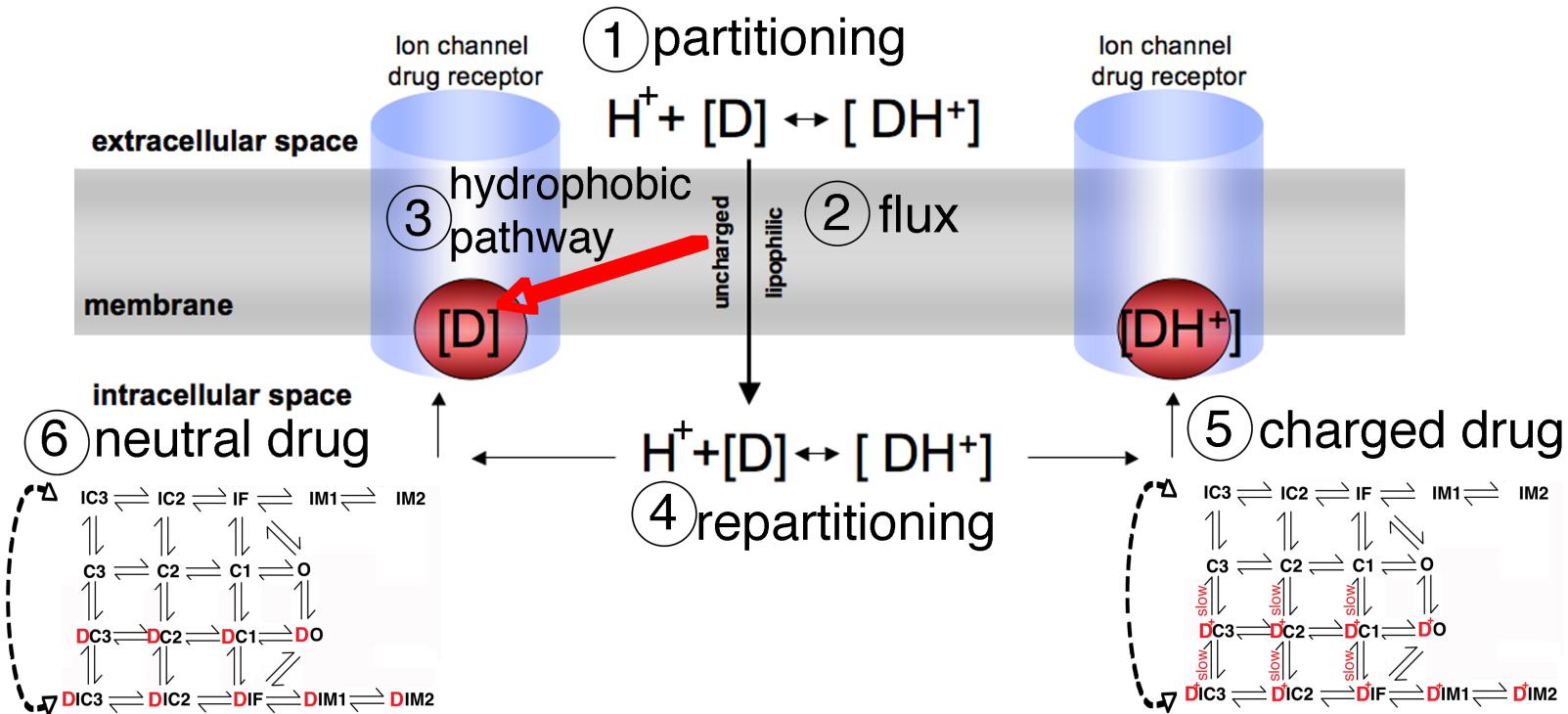


f.



Pharmacodynamics is Complex

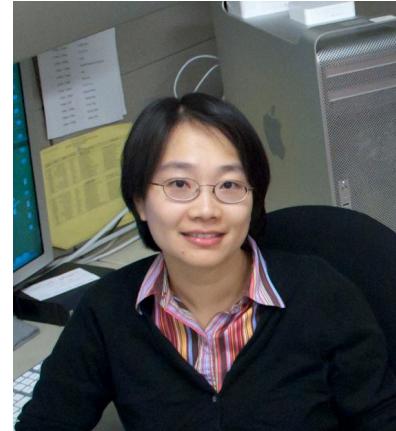
and determined by numerous factors including:



If we consider these properties in our model, can we begin to make predictions about functional effects of drug in higher dimensions?



Jonathan D. Moreno, M.D, Ph.D.



Pei-Chi Yang, Ph.D.

RESEARCH ARTICLE

DRUG DEVELOPMENT

A Computational Model to Predict the Effects of Class I Anti-Arrhythmic Drugs on Ventricular Rhythms



Jonathan D. Moreno,^{1,2} Z. Iris Zhu,² Pei-Chi Yang,³ John R. Bankston,⁴ Mao-Tsuen Jeng,³ Chaoyi Kang,³ Lianguo Wang,³ Jason D. Bayer,⁵ David J. Christini,² Natalia A. Trayanova,⁵ Crystal M. Ripplinger,³ Robert S. Kass,⁴ Colleen E. Clancy^{3*}

Circulation Research

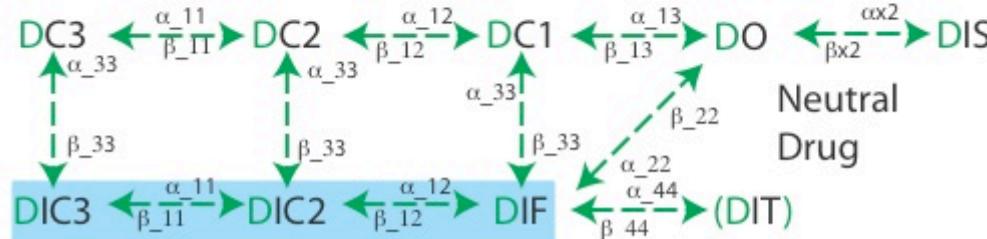
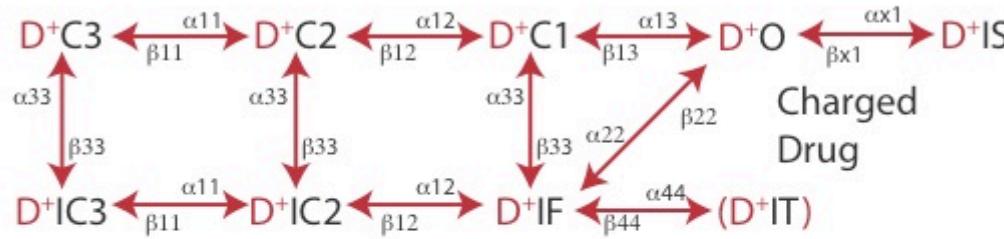
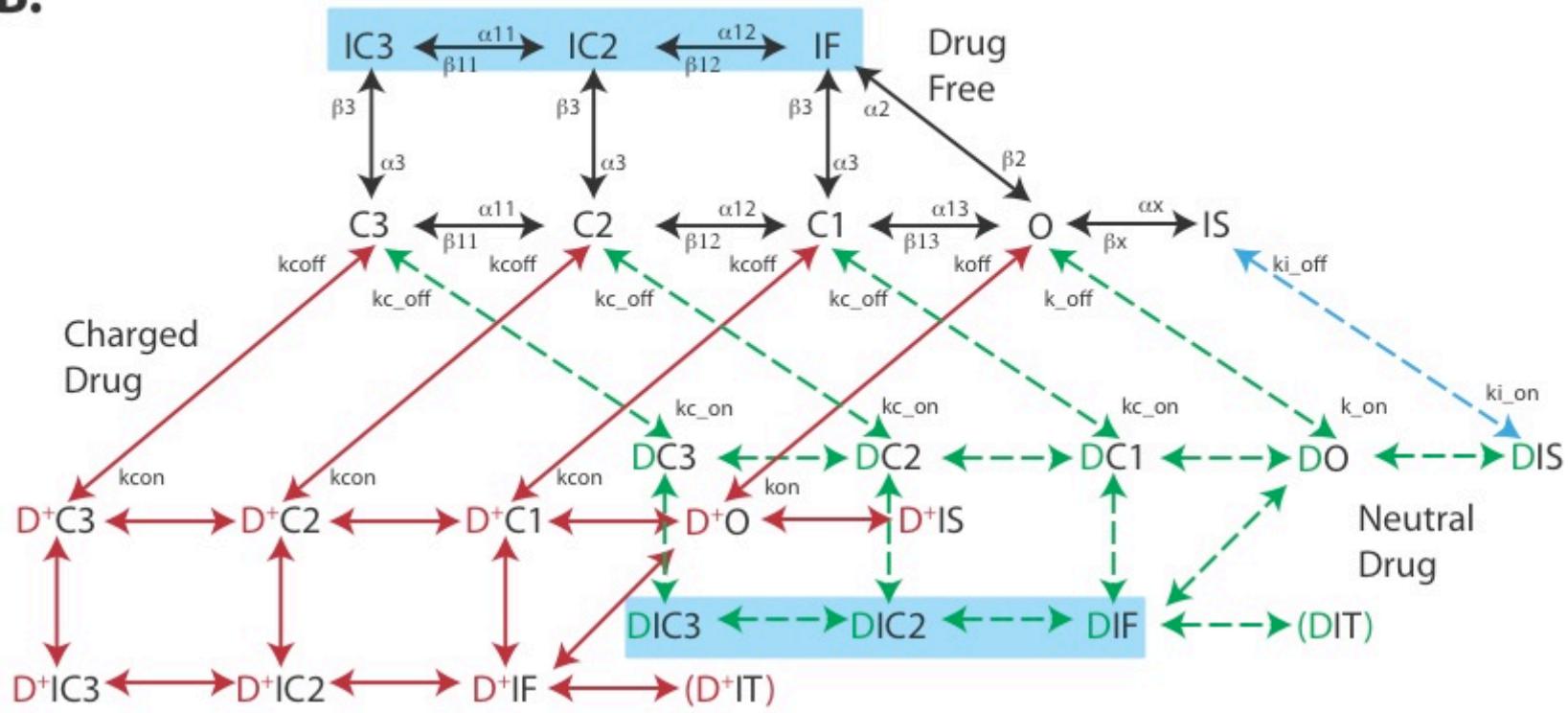
JOURNAL OF THE AMERICAN HEART ASSOCIATION



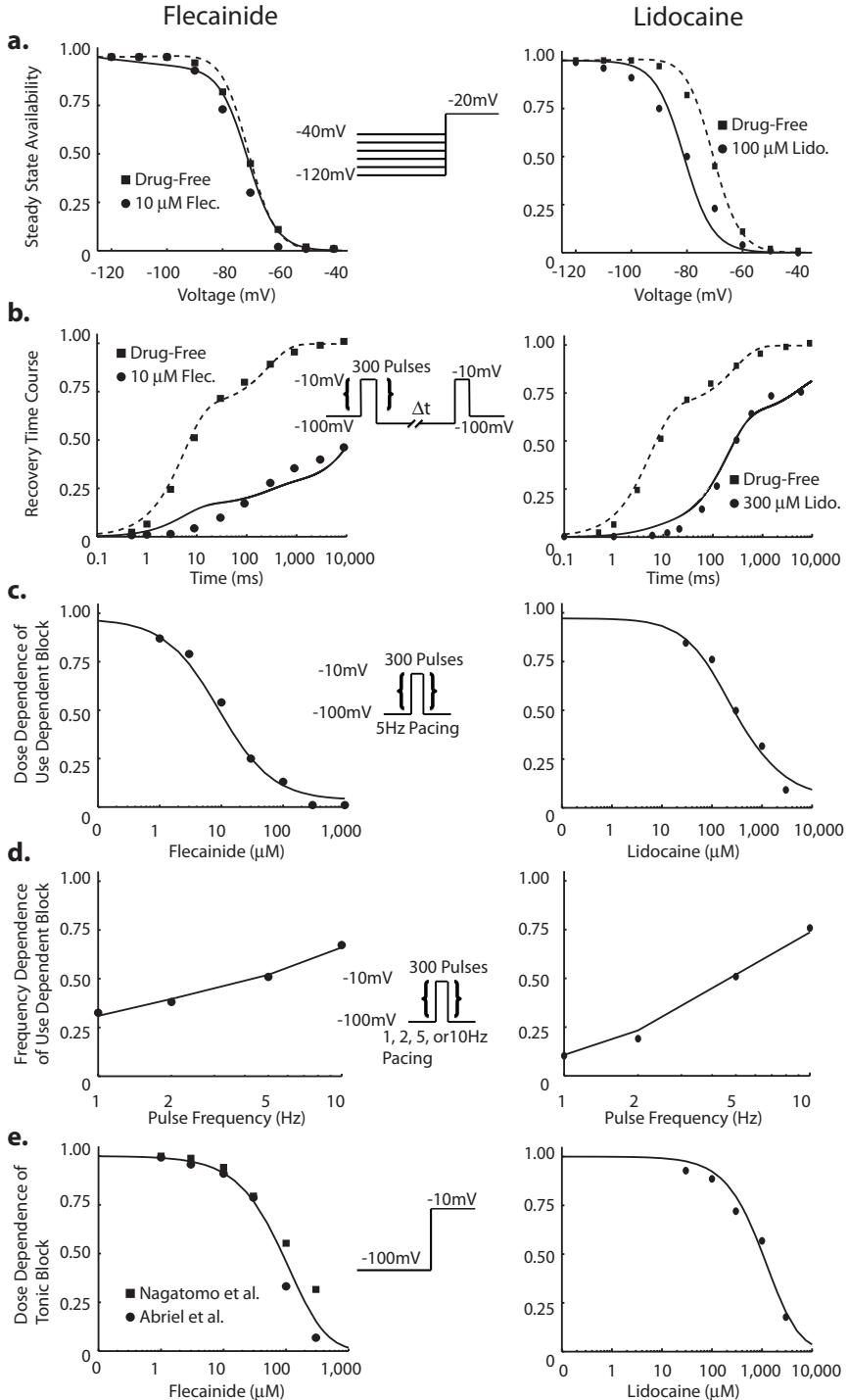
Ranolazine for Congenital and Acquired Late I_{Na} -Linked Arrhythmias: In Silico Pharmacological Screening

Jonathan D. Moreno, Pei-Chi Yang, John R. Bankston, Eleonora Grandi, Donald M. Bers,
Robert S. Kass and Colleen E. Clancy

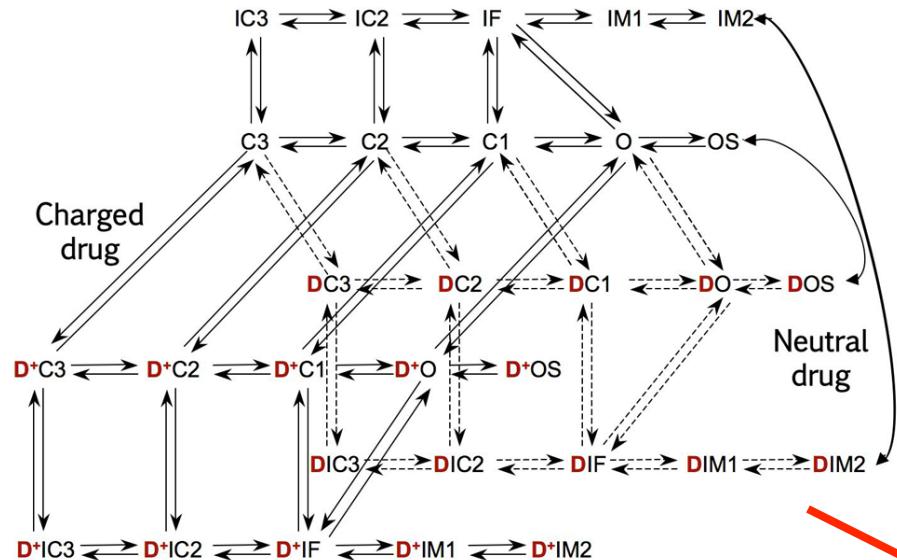
B.



Model fits to drug bound channel data



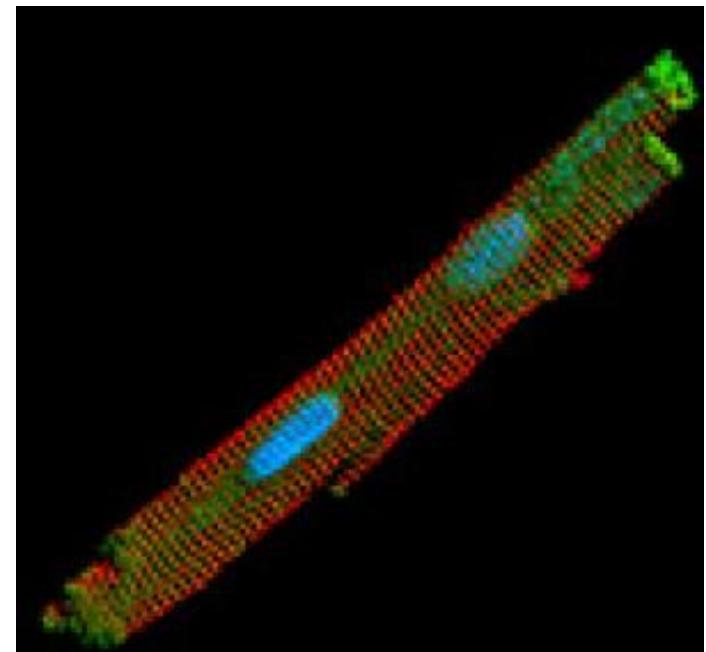
Drug Bound Channel



Predictions

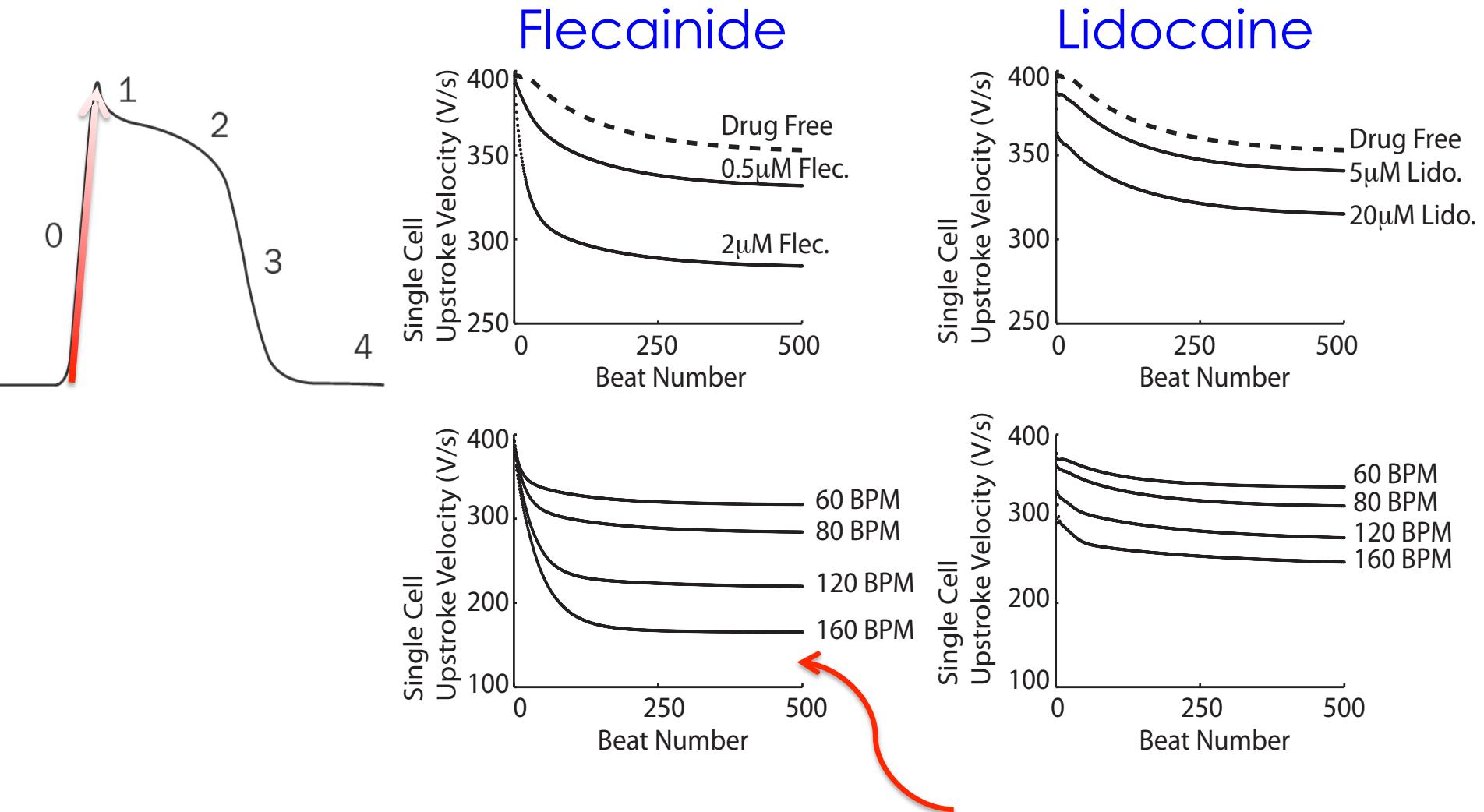
Simulations

Cardiac Cell Model



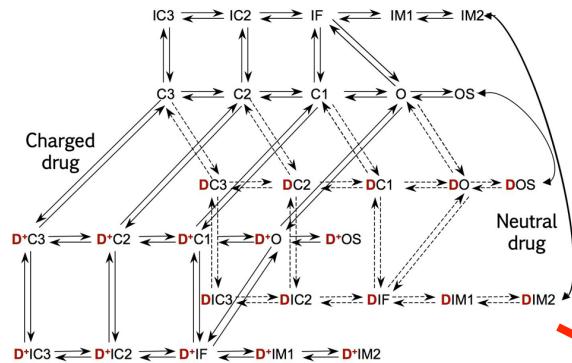
Picture from *ScienceDaily* - University of Iowa (2008, May 5). Heart Disease Discovery: New Mechanism Links Activation Of Key Heart Enzyme And Oxidative Stress.

Effects of drugs on *cell* excitability

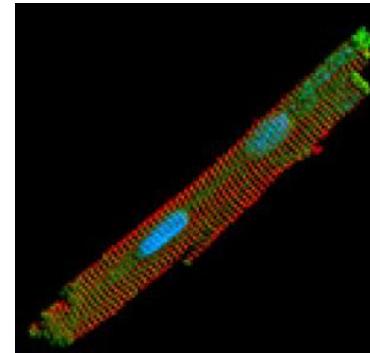


Increased Use-Dependent Block

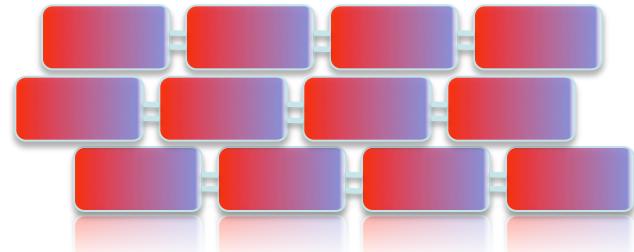
Drug Bound Channel



Cardiac Cell Model



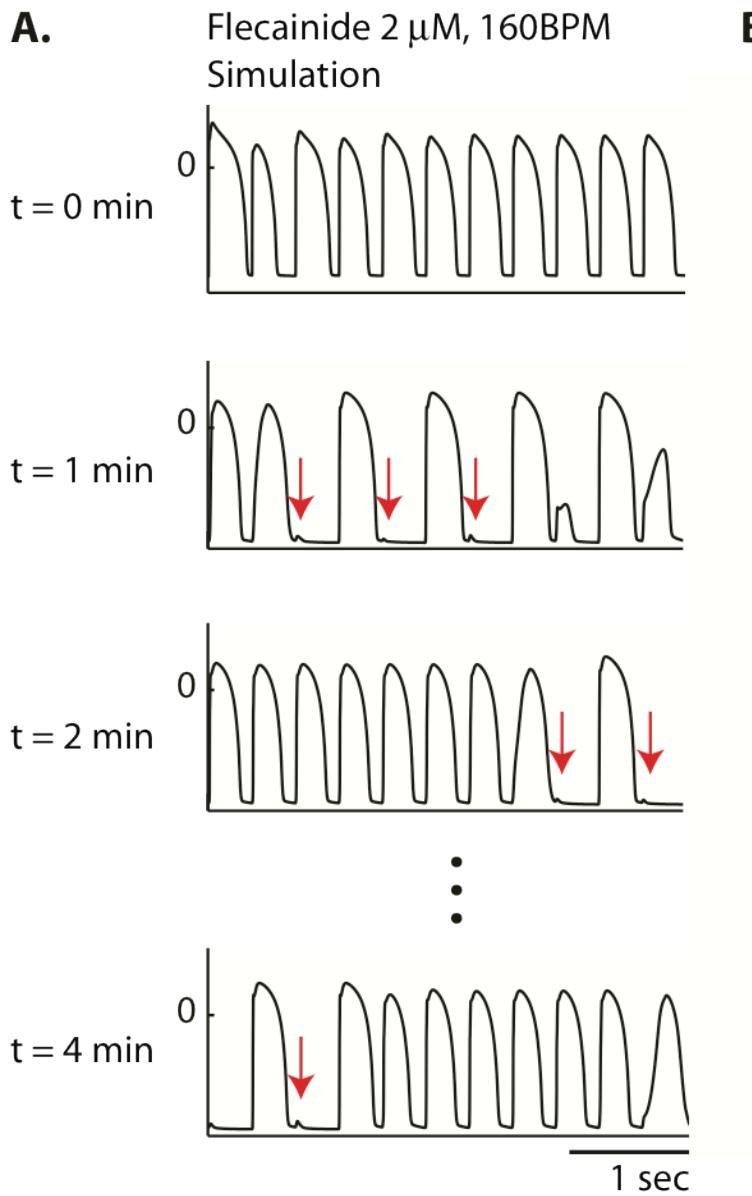
Multicellular Tissue



Picture from *ScienceDaily* - University of Iowa (2008, May 5). Heart Disease Discovery: New Mechanism Links Activation Of Key Heart Enzyme And Oxidative Stress.

Tissue level proarrhythmic conduction blocks: prediction and validation

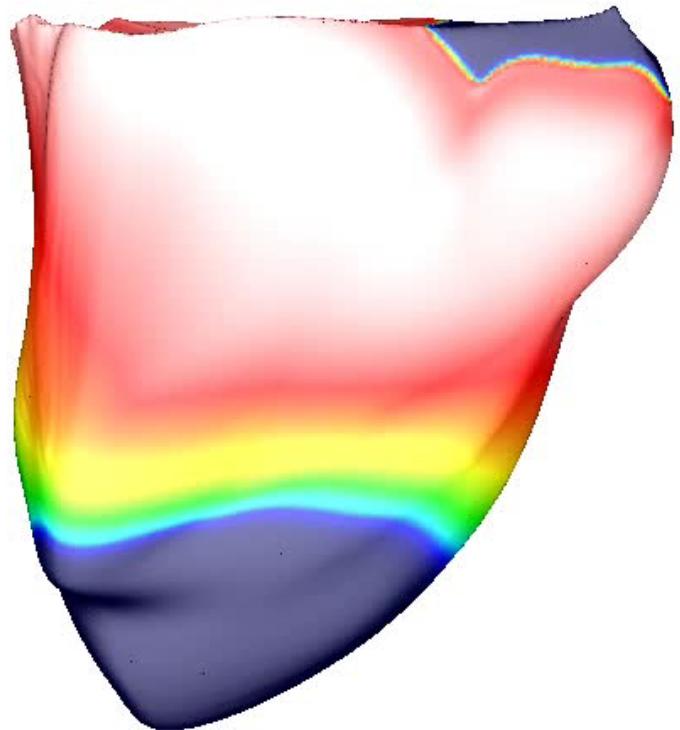
A.



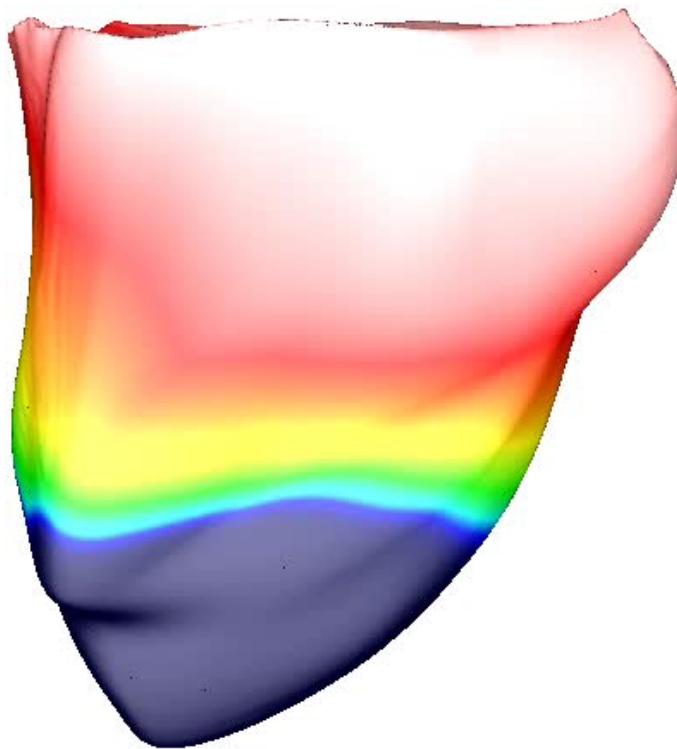
B

Drug effects on tissue dynamics

Persistent reentry
with flecainide



No reentry with
lidocaine



What's next?

Predictive multiscale computational pharmacology

Atomic to Organ

Computational EXPERIMENTS

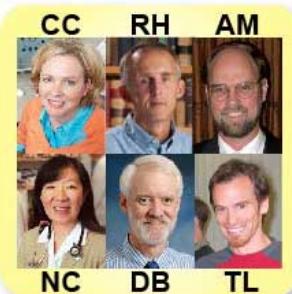
Team Members



NT AM

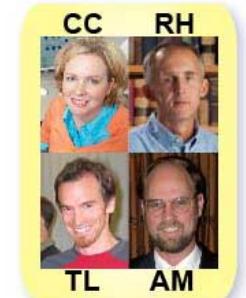


CC CR AM



CC RH AM

NC DB TL



CC RH

TL AM



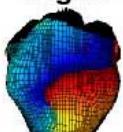
TA VYY



CC VYY

Scale

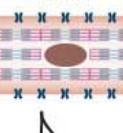
Organ



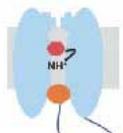
Tissue



Cell



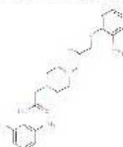
Ion Channel



Protein



Small Molecule



Space (meters)

10^{-2} m
 10^{-3} m
 10^{-6} m
 10^{-9} m
 10^{-10} m

Time (seconds)

10^{2} s
 10^0 s
 10^{-3} s
 10^{-9} s
 10^{-12} s

Methodology

Whole-Heart Simulations

1D, 2D Simulation
Optical Mapping

Ventricular Cell Model
Electrophysiology Expts.
 Ca^{2+} Imaging
iPS Cell Expts.

Markov Models
Patch Clamp
Reduced Models

Rosetta
Molecular Dynam.
Molecular Biol.
Expts.

What's next?

Development of a computational pharmacology working group as part of the MSM consortium.

ACKNOWLEDGEMENTS



National Institute of
General Medical Sciences



National Heart, Lung,
and Blood Institute



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www.clancylab.com

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Hank Duff (Calgary)
Lucia Romero Perez (Valencia)



The image shows a screenshot of a Facebook page for the "Clancy Lab". The cover photo features a 3D rendering of a brain with various colored regions and labels like "NH2", "NH3+", and "NH4+". Below the cover photo is a small thumbnail image of three people standing together. The page has 93 likes and 31 talking about it. A status update from Colleen Clancy reads: "Non-Profit Organization The Clancy Lab aims to develop and implement computational approaches to understand mechanisms of excitable disease in the heart and brain." At the bottom right, there are buttons for "Like", "Message", and "Photos".